

OM protein - protein search, using sw model

Run on: April 14, 2006, 20:39:58 ; Search time 190 Seconds  
(without alignments)  
1244.136 Million cell updates/sec

Title: US-10-796-669A-3  
Perfect score: 2769  
Sequence: 1 MTKKPARKILSFSTTMRNPK.....FIKKVENSIEWLQINDHLKA 538

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 14, 2006, 20:43:48 ; Search time 43 Seconds  
(without alignments)  
1203.828 Million cell updates/sec

Title: US-10-796-669A-3  
Perfect score: 2769  
Sequence: 1 MTKKPARKILSFSTTMRNPK.....FIKKVENSIEWLQINDHLKA 538

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pirl:\*

2: pir2:\*  
3: pir3:\*  
4: pir4:\*

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 14, 2006, 20:40:28 ; Search time 235 Seconds  
(without alignments)  
1615.209 Million cell updates/sec

Title: US-10-796-669A-3  
Perfect score: 2769  
Sequence: 1 MTKKPKARKILSFSTTMRNPK.....FIKKVENSIEWLQINDHLKA 538

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*